

Sequenzprotokoll

<110> Ernst-Moritz-Arndt Universität Greifswald

<120> Modulation der Insulinsynthese

<130> P 64322

<160> 12

<170> PatentIn version 3.1

<210> 1

<211> 852

<212> DNA

<213> Homo sapiens

<220>

<221> Stopcodon

<222> (850)..(852)

<223> Nukleotidsequenz von PDX-1

<400> 1

atgaacggcg aggagcagta ctacgcggcc acgcagcttt acaaggaccc atgcgcgttc	60
cagcgaggcc cggcgccgga gttcagcgcc agccccctg cgtgcctgta catgggccgc	120
cagccccgc cgccgccgcc gcacccgttc cctggcgccc tgggcgcgct ggagcagggc	180
agccccccgg acatctcccc gtacgaggtg cccccctcg ccgacgaccc cgcggtggcg	240
caccttcacc accacctccc ggctcagctc gcgctcccc acccgcccgc cgggcccttc	300
ccggagggag ccgagccggg cgtcctggag gagcccaacc gcgtccagct gcctttccca	360
tggatgaagt ctaccaaagc tcacgcgtgg aaaggccagt gggcaggcgg cgcctacgt	420
gcggagccgg aggagaacaa gcggacgcgc acggcctaca cgcgcgcaca gctgctagag	480
ctggagaagg agttcctatt caacaagtac atctcacggc cgcgccgggt ggagctggct	540
gtcatgttga acttgaccga gagacacatc aagatctggt tccaaaaccg ccgcatgaag	600
tggaaaaagg aggaggacaa gaagcgcggc ggcgggacag ctgtcggggg tggcggggtc	660
gcggagcctg agcaggactg cgcctgacc tccggcgagg agcttctggc gctgccgccg	720
ccgcccccc ccggaggtgc tgtgccgcc gctgcccccg ttgccgccg agagggccgc	780
ctgccgcctg gccttagcgc gtcgccacag ccctccagcg tcgcgcctcg gcggccgcag	840
gaaccacgat ga	852

<210> 2
 <211> 283
 <212> PRT
 <213> Homo sapiens

<223> Aminosäuresequenz von PDX-1

<400> 2

Met Asn Gly Glu Glu Gln Tyr Tyr Ala Ala Thr Gln Leu Tyr Lys Asp
 1 5 10 15

Pro Cys Ala Phe Gln Arg Gly Pro Ala Pro Glu Phe Ser Ala Ser Pro
 20 25 30

Pro Ala Cys Leu Tyr Met Gly Arg Gln Pro Pro Pro Pro Pro Pro His
 35 40 45

Pro Phe Pro Gly Ala Leu Gly Ala Leu Glu Gln Gly Ser Pro Pro Asp
 50 55 60

Ile Ser Pro Tyr Glu Val Pro Pro Leu Ala Asp Asp Pro Ala Val Ala
 65 70 75 80

His Leu His His His Leu Pro Ala Gln Leu Ala Leu Pro His Pro Pro
 85 90 95

Ala Gly Pro Phe Pro Glu Gly Ala Glu Pro Gly Val Leu Glu Glu Pro
 100 105 110

Asn Arg Val Gln Leu Pro Phe Pro Trp Met Lys Ser Thr Lys Ala His
 115 120 125

Ala Trp Lys Gly Gln Trp Ala Gly Gly Ala Tyr Ala Ala Glu Pro Glu
 130 135 140

Glu Asn Lys Arg Thr Arg Thr Ala Tyr Thr Arg Ala Gln Leu Leu Glu
 145 150 155 160

Leu Glu Lys Glu Phe Leu Phe Asn Lys Tyr Ile Ser Arg Pro Arg Arg
 165 170 175

Val Glu Leu Ala Val Met Leu Asn Leu Thr Glu Arg His Ile Lys Ile
 180 185 190

Trp Phe Gln Asn Arg Arg Met Lys Trp Lys Lys Glu Glu Asp Lys Lys
 195 200 205

Arg Gly Gly Gly Thr Ala Val Gly Gly Gly Gly Val Ala Glu Pro Glu
 210 215 220

Gln Asp Cys Ala Val Thr Ser Gly Glu Glu Leu Leu Ala Leu Pro Pro
225 230 235 240

Pro Pro Pro Pro Gly Gly Ala Val Pro Pro Ala Ala Pro Val Ala Ala
245 250 255

Arg Glu Gly Arg Leu Pro Pro Gly Leu Ser Ala Ser Pro Gln Pro Ser
260 265 270

Ser Val Ala Pro Arg Arg Pro Gln Glu Pro Arg
275 280

<210> 3

<211> 1182

<212> DNA

<213> Homo sapiens

<220>

<221> Stopcodon

<222> (1080)..(1082)

<223> Nukleotidsequenz von CKII-Untereinheit alpha

<400> 3

atgtcgggac ccgtgccaag cagggccaga gtttacacag atgttaatac acacagacct 60
cgagaatact gggattacga gtcacatgtg gtggaatggg gaaatcaaga tgactaccag 120
ctgggttcgaa aattaggccg aggtaaatac agtgaagtat ttgaagccat caacatcaca 180
aataatgaaa aagttgttgt taaaattctc aagccagtaa aaaagaagaa aattaagcgt 240
gaaataaaga ttttgagaaa tttgagagga ggtccaaca tcatcacact ggcagacatt 300
gtaaaagacc ctgtgtcacg aacccccgcc ttgggttttg aacacgtaaa caacacagac 360
ttcaagcaat tgtaccagac gttaacagac tatgatattc gattttacat gtatgagatt 420
ctgaaggccc tggattattg tcacagcatg ggaattatgc acagagatgt caagccccat 480
aatgtcatga ttgatcatga gcacagaaaag ctacgactaa tagactgggg tttggctgag 540
ttttatcatc ctggccaaga atataatgtc cgagttgctt cccgatactt caaaggctct 600
gagctacttg tagactatca gatgtacgat tatagtttgg atatgtggag tttgggttgt 660
atgctggcaa gtatgatctt tcggaaggag ccatttttcc atggacatga caattatgat 720
cagttggtga ggatagccaa gggtctgggg acagaagatt tatatgacta tattgacaaa 780
tacaacattg aattagatcc acgtttcaat gatatcttgg gcagacactc tcgaaagcga 840
tggaacgct ttgtccacag tgaaaatcag caccttgtca gccctgaggc cttggatttc 900
ctggacaaac tgctgcgata tgaccaccag tcacggctta ctgcaagaga ggcaatggag 960
caccctatt tctacactgt tgtgaaggac caggctcgaa tgggttcac tagcatgcc 1020

gggggacagta cgcccgtag cagcgccaat atgatgtcag ggatttcttc agtgccaacc 1080
ccttcacccc ttggacctct ggcaggctca ccagtgattg ctgctgccaa ccccttggg 1140
atgcctgttc cagctgccgc tggcgctcag cagtaacggc cc 1182

<210> 4

<211> 391

<212> PRT

<213> Homo sapiens

<223> Aminosäuresequenz von CKII-Untereinheit alpha

<400> 4

Met Ser Gly Pro Val Pro Ser Arg Ala Arg Val Tyr Thr Asp Val Asn
1 5 10 15

Thr His Arg Pro Arg Glu Tyr Trp Asp Tyr Glu Ser His Val Val Glu
20 25 30

Trp Gly Asn Gln Asp Asp Tyr Gln Leu Val Arg Lys Leu Gly Arg Gly
35 40 45

Lys Tyr Ser Glu Val Phe Glu Ala Ile Asn Ile Thr Asn Asn Glu Lys
50 55 60

Val Val Val Lys Ile Leu Lys Pro Val Lys Lys Lys Lys Ile Lys Arg
65 70 75 80

Glu Ile Lys Ile Leu Glu Asn Leu Arg Gly Gly Pro Asn Ile Ile Thr
85 90 95

Leu Ala Asp Ile Val Lys Asp Pro Val Ser Arg Thr Pro Ala Leu Val
100 105 110

Phe Glu His Val Asn Asn Thr Asp Phe Lys Gln Leu Tyr Gln Thr Leu
115 120 125

Thr Asp Tyr Asp Ile Arg Phe Tyr Met Tyr Glu Ile Leu Lys Ala Leu
130 135 140

Asp Tyr Cys His Ser Met Gly Ile Met His Arg Asp Val Lys Pro His
145 150 155 160

Asn Val Met Ile Asp His Glu His Arg Lys Leu Arg Leu Ile Asp Trp
165 170 175

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Gly Leu Ala Glu Phe Tyr His Pro Gly Gln Glu Tyr Asn Val Arg Val
 180 185 190

Ala Ser Arg Tyr Phe Lys Gly Pro Glu Leu Leu Val Asp Tyr Gln Met
 195 200 205

Tyr Asp Tyr Ser Leu Asp Met Trp Ser Leu Gly Cys Met Leu Ala Ser
 210 215 220

Met Ile Phe Arg Lys Glu Pro Phe Phe His Gly His Asp Asn Tyr Asp
 225 230 235 240

Gln Leu Val Arg Ile Ala Lys Val Leu Gly Thr Glu Asp Leu Tyr Asp
 245 250 255

Tyr Ile Asp Lys Tyr Asn Ile Glu Leu Asp Pro Arg Phe Asn Asp Ile
 260 265 270

Leu Gly Arg His Ser Arg Lys Arg Trp Glu Arg Phe Val His Ser Glu
 275 280 285

Asn Gln His Leu Val Ser Pro Glu Ala Leu Asp Phe Leu Asp Lys Leu
 290 295 300

Leu Arg Tyr Asp His Gln Ser Arg Leu Thr Ala Arg Glu Ala Met Glu
 305 310 315 320

His Pro Tyr Phe Tyr Thr Val Val Lys Asp Gln Ala Arg Met Gly Ser
 325 330 335

Ser Ser Met Pro Gly Gly Ser Thr Pro Val Ser Ser Ala Asn Met Met
 340 345 350

Ser Gly Ile Ser Ser Val Pro Thr Pro Ser Pro Leu Gly Pro Leu Ala
 355 360 365

Gly Ser Pro Val Ile Ala Ala Ala Asn Pro Leu Gly Met Pro Val Pro
 370 375 380

Ala Ala Ala Gly Ala Gln Gln
 385 390

<210> 5
 <211> 1053
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> Stopcodon
 <222> (1051)..(1053)
 <223> Nukleotidsequenz von CKII-Untereinheit alpha'

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<400> 5
atgcccggcc cggccgcggg cagcagggcc cgggtctacg ccgaggtgaa cagtctgagg      60
agccgcgagt actgggacta cgaggctcac gtcccgagct ggggtaatca agatgattac      120
caactggttc gaaaacttgg tcggggaaaa tatagtgaag tatttgaggc cattaatatc      180
accaacaatg agagagtggg tgtaaaaatc ctgaagccag tgaagaaaaa gaagataaaa      240
cgagaggtta agattctgga gaaccttcgt ggtggaacaa atatcattaa gctgattgac      300
actgtaaagg accccgtgtc aaagacacca gctttgggat ttgaatatat caataatata      360
gattttaagc aactctacca gatcctgaca gactttgata tccggtttta tatgtatgaa      420
ctacttaaag ctctggatta ctgccacagc aagggaatca tgcacagggg tgtgaaacct      480
cacaatgtca tgatagatca ccaacagaaa aagctgcgac tgatagattg gggctctggca      540
gaattctatc atcctgctca ggagtacaat gttcgtgtag cctcaaggta cttcaaggga      600
ccagagctcc tcgtggacta tcagatgtat gattatagct tggacatgtg gagtttgggc      660
tgtatgttag caagcatgat ctttcgaagg gaaccattct tccatggaca ggacaactat      720
gaccagcttg ttcgcattgc caaggttctg ggtacagaag aactgtatgg gtatctgaag      780
aagtatcaca tagacctaga tccacacttc aacgatatcc tgggacaaca ttcacggaaa      840
cgctgggaaa actttatcca tagtgagaac agacaccttg tcagccctga ggccctagat      900
cttctggaca aacttctgcg atacgaccat caacagagac tgactgccaa agaggccatg      960
gagcaccat acttctaccc tgtggggaag gagcagtcce agccttgtgc agacaatgct     1020
gtgctttcca gtggtctcac ggcagcacga tga                                     1053
  
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<210> 6
 <211> 350
 <212> PRT
 <213> Homo sapiens

 <223> Aminosäuresequenz von CKII-Untereinheit alpha'

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<400> 6
Met Pro Gly Pro Ala Ala Gly Ser Arg Ala Arg Val Tyr Ala Glu Val
1           5           10          15
  
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Asn Ser Leu Arg Ser Arg Glu Tyr Trp Asp Tyr Glu Ala His Val Pro
20 25 30

Ser Trp Gly Asn Gln Asp Asp Tyr Gln Leu Val Arg Lys Leu Gly Arg
35 40 45

Gly Lys Tyr Ser Glu Val Phe Glu Ala Ile Asn Ile Thr Asn Asn Glu
50 55 60

Arg Val Val Val Lys Ile Leu Lys Pro Val Lys Lys Lys Lys Ile Lys
65 70 75 80

Arg Glu Val Lys Ile Leu Glu Asn Leu Arg Gly Gly Thr Asn Ile Ile
85 90 95

Lys Leu Ile Asp Thr Val Lys Asp Pro Val Ser Lys Thr Pro Ala Leu
100 105 110

Val Phe Glu Tyr Ile Asn Asn Thr Asp Phe Lys Gln Leu Tyr Gln Ile
115 120 125

Leu Thr Asp Phe Asp Ile Arg Phe Tyr Met Tyr Glu Leu Leu Lys Ala
130 135 140

Leu Asp Tyr Cys His Ser Lys Gly Ile Met His Arg Asp Val Lys Pro
145 150 155 160

His Asn Val Met Ile Asp His Gln Gln Lys Lys Leu Arg Leu Ile Asp
165 170 175

Trp Gly Leu Ala Glu Phe Tyr His Pro Ala Gln Glu Tyr Asn Val Arg
180 185 190

Val Ala Ser Arg Tyr Phe Lys Gly Pro Glu Leu Leu Val Asp Tyr Gln
195 200 205

Met Tyr Asp Tyr Ser Leu Asp Met Trp Ser Leu Gly Cys Met Leu Ala
210 215 220

Ser Met Ile Phe Arg Arg Glu Pro Phe Phe His Gly Gln Asp Asn Tyr
225 230 235 240

Asp Gln Leu Val Arg Ile Ala Lys Val Leu Gly Thr Glu Glu Leu Tyr
245 250 255

Gly Tyr Leu Lys Lys Tyr His Ile Asp Leu Asp Pro His Phe Asn Asp
260 265 270

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Ile Leu Gly Gln His Ser Arg Lys Arg Trp Glu Asn Phe Ile His Ser
 275 280 285

Glu Asn Arg His Leu Val Ser Pro Glu Ala Leu Asp Leu Leu Asp Lys
 290 295 300

Leu Leu Arg Tyr Asp His Gln Gln Arg Leu Thr Ala Lys Glu Ala Met
 305 310 315 320

Glu His Pro Tyr Phe Tyr Pro Val Val Lys Glu Gln Ser Gln Pro Cys
 325 330 335

Ala Asp Asn Ala Val Leu Ser Ser Gly Leu Thr Ala Ala Arg
 340 345 350

<210> 7
 <211> 648
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Stopcodon
 <222> (646)..(648)
 <223> Nukleotidsequenz von CKII-Untereinheit beta

<400> 7
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 ttcttctgtg aagtggatga agactacatc caggacaaat ttaatcttac tggactcaat 120
 gaggaggtcc ctactatcgc acaagctcta gacatgatct tggacctgga gcctgatgaa 180
 gaactggaag acaaccccaa ccagagtgac ctgattgagc aggcagccga gatgctttat 240
 ggattgatcc acgcccgcga catccttacc aaccgtggca tcgcccagat gttggaaaag 300
 taccagcaag gagactttgg ttactgtcct cgtgtgtact gtgagaacca gccaatgctt 360
 cccattggcc ttccagacat cccaggtgaa gccatggtga agctctactg ccccaagtgc 420
 atggatgtgt acacacccaa gtcacaaaga caccatcaca cggatggcgc ctacttcggc 480
 actggtttcc ctacatgctt cttcatggtg catcccgagt accggcccaa gagacctgcc 540
 aaccagtttg tgcccaggct ctacggtttc aagatccatc cgatggccta ccagctgcag 600
 ctccaagccg ccagcaactt caagagccca gtcaagacga ttcgctga 648

<210> 8

<211> 215

<212> PRT

<213> Homo sapiens.

<223> Aminosäuresequenz von CKII-Untereinheit beta

<400> 8

Met Ser Ser Ser Glu Glu Val Ser Trp Ile Ser Trp Phe Cys Gly Leu
1 5 10 15

Arg Gly Asn Glu Phe Phe Cys Glu Val Asp Glu Asp Tyr Ile Gln Asp
20 25 30

Lys Phe Asn Leu Thr Gly Leu Asn Glu Gln Val Pro His Tyr Arg Gln
35 40 45

Ala Leu Asp Met Ile Leu Asp Leu Glu Pro Asp Glu Glu Leu Glu Asp
50 55 60

Asn Pro Asn Gln Ser Asp Leu Ile Glu Gln Ala Ala Glu Met Leu Tyr
65 70 75 80

Gly Leu Ile His Ala Arg Tyr Ile Leu Thr Asn Arg Gly Ile Ala Gln
85 90 95

Met Leu Glu Lys Tyr Gln Gln Gly Asp Phe Gly Tyr Cys Pro Arg Val
100 105 110

Tyr Cys Glu Asn Gln Pro Met Leu Pro Ile Gly Leu Ser Asp Ile Pro
115 120 125

Gly Glu Ala Met Val Lys Leu Tyr Cys Pro Lys Cys Met Asp Val Tyr
130 135 140

Thr Pro Lys Ser Ser Arg His His His Thr Asp Gly Ala Tyr Phe Gly
145 150 155 160

Thr Gly Phe Pro His Met Leu Phe Met Val His Pro Glu Tyr Arg Pro
165 170 175

Lys Arg Pro Ala Asn Gln Phe Val Pro Arg Leu Tyr Gly Phe Lys Ile
180 185 190

His Pro Met Ala Tyr Gln Leu Gln Leu Gln Ala Ala Ser Asn Phe Lys
195 200 205

Ser Pro Val Lys Thr Ile Arg
210 215

<210> 9
<211> 768
<212> DNA
<213> Homo sapiens

<220>
<221> Stopcodon
<222> (766)..(768)
<223> Nukleotidsequenz von 14-3-3 epsilon

<400> 9
atggatgatac gagaggatct ggtgtaccag gcgaagctgg ccgagcaggc tgagcgatac 60
gacgaaatgg tggagtcaat gaagaaagta gcagggatgg atgtggagct gacagttgaa 120
gaaagaaacc tcctatctgt tgcataaag aatgtgattg gagctagaag agcctcctgg 180
agaataatca gcagcattga acagaaagaa gaaaacaagg gaggagaaga caagctaaaa 240
atgattcggg aatatcggca aatggttgag actgagctaa agttaatctg ttgtgacatt 300
ctggatgtac tggacaaaca cctcattcca gcagctaaca ctggcgagtc caagggttttc 360
tattataaaa tgaaagggga ctaccacagg tatctggcag aatttgccac aggaaacgac 420
aggaaggagg ctgcggagaa cagcctagtg gcttataaag ctgctagtga tattgcaatg 480
acagaacttc caccaacgca tcctattcgc ttaggtcttg ctctcaattt ttccgtattc 540
tactacgaaa ttcttaattc ccctgaccgt gcctgcaggt tggcaaaagc agctttttgat 600
gatgcaattg cagaactgga tacgctgagt gaagaaagct ataaggactc tacacttatc 660
atgcagttgt tacgtgataa tctgacacta tggacttcag acatgcaggg tgacgggtgaa 720
gagcagaata aagaagcgcg gcaggacgtg gaagacgaaa atcagtgga 768

<210> 10
<211> 255
<212> PRT
<213> Homo sapiens

<223> Aminosäuresequenz von 14-3-3 epsilon

<400> 10
Met Asp Asp Arg Glu Asp Leu Val Tyr Gln Ala Lys Leu Ala Glu Gln
1 5 10 15
Ala Glu Arg Tyr Asp Glu Met Val Glu Ser Met Lys Lys Val Ala Gly
20 25 30

Met Asp Val Glu Leu Thr Val Glu Glu Arg Asn Leu Leu Ser Val Ala
35 40 45

Tyr Lys Asn Val Ile Gly Ala Arg Arg Ala Ser Trp Arg Ile Ile Ser
50 55 60

Ser Ile Glu Gln Lys Glu Glu Asn Lys Gly Gly Glu Asp Lys Leu Lys
65 70 75 80

Met Ile Arg Glu Tyr Arg Gln Met Val Glu Thr Glu Leu Lys Leu Ile
85 90 95

Cys Cys Asp Ile Leu Asp Val Leu Asp Lys His Leu Ile Pro Ala Ala
100 105 110

Asn Thr Gly Glu Ser Lys Val Phe Tyr Tyr Lys Met Lys Gly Asp Tyr
115 120 125

His Arg Tyr Leu Ala Glu Phe Ala Thr Gly Asn Asp Arg Lys Glu Ala
130 135 140

Ala Glu Asn Ser Leu Val Ala Tyr Lys Ala Ala Ser Asp Ile Ala Met
145 150 155 160

Thr Glu Leu Pro Pro Thr His Pro Ile Arg Leu Gly Leu Ala Leu Asn
165 170 175

Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Pro Asp Arg Ala Cys
180 185 190

Arg Leu Ala Lys Ala Ala Phe Asp Asp Ala Ile Ala Glu Leu Asp Thr
195 200 205

Leu Ser Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln Leu Leu
210 215 220

Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Met Gln Gly Asp Gly Glu
225 230 235 240

Glu Gln Asn Lys Glu Ala Leu Gln Asp Val Glu Asp Glu Asn Gln
245 250 255

<210> 11
 <211> 1284
 <212> DNA
 <213> Homo sapiens.

<220>
 <221> Stopcodon
 <222> (1282)..(1284)
 <223> Nukleotidsequenz der kurzen Isoform von EED

<400> 11
 atgcctgcgg ccaagaagca gaagctgagc agtgacgaga acagcaatcc agaactctct 60
 ggagacgaga atgatgacgc tgtcagtata gaaagtggta caaacactga acgccctgat 120
 acacctacaa acacgccaaa tgcacctgga aggaaaagtt ggggaaaggg aaaatggaag 180
 tcaaagaaat gcaaattattc tttcaaattgt gtaaattagtc tcaaggaaga tcataaccaa 240
 ccattgtttg gagttcagtt taactggcac agtaaagaag gagatccatt agtgtttgca 300
 actgtaggaa gcaacagagt taccttgtat gaatgtcatt cacaaggaga aatccggttg 360
 ttgcaatctt acgtggatgc tgatgctgat gaaaactttt acacttgtgc atggacctat 420
 gatagcaata cgagccatcc tctgctggct gtagctggat ctagaggcat aattaggata 480
 ataaatccta taacaatgca gtgtataaag cactatgttg gccatggaaa tgctatcaat 540
 gagctgaaat tccatccaag agatccaaat cttctcctgt cagtaagtaa agatcatgct 600
 ttacgattat ggaatatcca gacggacact ctggtggcaa tatttggagg cgtagaaggg 660
 cacagagatg aagttctaag tgctgattat gatcttttgg gtgaaaaaat aatgtcctgt 720
 ggtatggatc attctcttaa acttttggagg atcaattcaa agagaatgat gaatgcaatt 780
 aaggaatctt atgattataa tccaaataaa actaacaggc catttatttc tcagaaaatc 840
 cattttcctg atttttctac cagagacata cataggaatt atgttgattg tgtgcgatgg 900
 ttaggcgatt tgatactttc taagtcttgt gaaaatgcca ttgtgtgctg gaaacctggc 960
 aagatggaag atgatataga taaaattaaa ccagtgtaat ctaatgtgac tattcttggg 1020
 cgatttgatt acagccagtg tgacatttgg tacatgaggt tttctatgga tttctggcaa 1080
 aagatgcttg cattgggcaa tcaagttggc aaactttatg tttgggattt agaagtagaa 1140
 gatcctcata aagccaaatg tacaacactg actcatcata aatgtggtgc tgctattcga 1200
 caaaccagtt ttagcagggg tagcagcatt cttatagctg tttgtgatga tgccagtatt 1260
 tggcgctggg atcgacttcg ataa 1284

<210> 12
<211> 427
<212> PRT
<213> Homo sapiens

<223> Aminosäuresequenz der kurzen Isoform von EED

<400> 12

Met Pro Ala Ala Lys Lys Gln Lys Leu Ser Ser Asp Glu Asn Ser Asn
1 5 10 15

Pro Glu Leu Ser Gly Asp Glu Asn Asp Asp Ala Val Ser Ile Glu Ser
20 25 30

Gly Thr Asn Thr Glu Arg Pro Asp Thr Pro Thr Asn Thr Pro Asn Ala
35 40 45

Pro Gly Arg Lys Ser Trp Gly Lys Gly Lys Trp Lys Ser Lys Lys Cys
50 55 60

Lys Tyr Ser Phe Lys Cys Val Asn Ser Leu Lys Glu Asp His Asn Gln
65 70 75 80

Pro Leu Phe Gly Val Gln Phe Asn Trp His Ser Lys Glu Gly Asp Pro
85 90 95

Leu Val Phe Ala Thr Val Gly Ser Asn Arg Val Thr Leu Tyr Glu Cys
100 105 110

His Ser Gln Gly Glu Ile Arg Leu Leu Gln Ser Tyr Val Asp Ala Asp
115 120 125

Ala Asp Glu Asn Phe Tyr Thr Cys Ala Trp Thr Tyr Asp Ser Asn Thr
130 135 140

Ser His Pro Leu Leu Ala Val Ala Gly Ser Arg Gly Ile Ile Arg Ile
145 150 155 160

Ile Asn Pro Ile Thr Met Gln Cys Ile Lys His Tyr Val Gly His Gly
165 170 175

Asn Ala Ile Asn Glu Leu Lys Phe His Pro Arg Asp Pro Asn Leu Leu
180 185 190

Leu Ser Val Ser Lys Asp His Ala Leu Arg Leu Trp Asn Ile Gln Thr
195 200 205

Asp Thr Leu Val Ala Ile Phe Gly Gly Val Glu Gly His Arg Asp Glu
210 215 220

Val Leu Ser Ala Asp Tyr Asp Leu Leu Gly Glu Lys Ile Met Ser Cys
225 230 235 240

Gly Met Asp His Ser Leu Lys Leu Trp Arg Ile Asn Ser Lys Arg Met
245 250 255

Met Asn Ala Ile Lys Glu Ser Tyr Asp Tyr Asn Pro Asn Lys Thr Asn
260 265 270

Arg Pro Phe Ile Ser Gln Lys Ile His Phe Pro Asp Phe Ser Thr Arg
275 280 285

Asp Ile His Arg Asn Tyr Val Asp Cys Val Arg Trp Leu Gly Asp Leu
290 295 300

Ile Leu Ser Lys Ser Cys Glu Asn Ala Ile Val Cys Trp Lys Pro Gly
305 310 315 320

Lys Met Glu Asp Asp Ile Asp Lys Ile Lys Pro Ser Glu Ser Asn Val
325 330 335

Thr Ile Leu Gly Arg Phe Asp Tyr Ser Gln Cys Asp Ile Trp Tyr Met
340 345 350

Arg Phe Ser Met Asp Phe Trp Gln Lys Met Leu Ala Leu Gly Asn Gln
355 360 365

Val Gly Lys Leu Tyr Val Trp Asp Leu Glu Val Glu Asp Pro His Lys
370 375 380

Ala Lys Cys Thr Thr Leu Thr His His Lys Cys Gly Ala Ala Ile Arg
385 390 395 400

Gln Thr Ser Phe Ser Arg Asp Ser Ser Ile Leu Ile Ala Val Cys Asp
405 410 415

Asp Ala Ser Ile Trp Arg Trp Asp Arg Leu Arg
420 425